

L Number	Hits	Search Text	DB	Time stamp
1	1	"6291174" .pn.	USPAT; US-PGPUB	2002/05/15 16:33
2	2874	fsh or (follicle near3 stimulating)	USPAT; US-PGPUB	2002/05/15 16:34
3	1	("6291174" .pn.) and (pig porcine)	USPAT; US-PGPUB	2002/05/15 16:35
4	1	("6291174" .pn.) and (swine)	USPAT; US-PGPUB	2002/05/15 16:35
5	1	("6291174" .pn.) and litter	USPAT; US-PGPUB	2002/05/15 16:35

L Number	Hits	Search Text	DB	Time stamp
1	1	"6291174" .pn.	USPAT; US-PGPUB	2002/05/15 16:33
2	2874	fsh or (follicle near3 stimulating)	USPAT; US-PGPUB	2002/05/15 16:37
3	1	("6291174" .pn.) and (pig porcine)	USPAT; US-PGPUB	2002/05/15 16:35
4	1	("6291174" .pn.) and (swine)	USPAT; US-PGPUB	2002/05/15 16:35
5	1	("6291174" .pn.) and litter	USPAT; US-PGPUB	2002/05/15 16:35
6	1038	(fsh or (follicle near3 stimulating)) and (pig porcine swine litter)	USPAT; US-PGPUB	2002/05/15 16:36
7	1029	(fsh or (follicle near3 stimulating)) and (pig porcine swine)	USPAT; US-PGPUB	2002/05/15 16:36
8	335	(fsh or (follicle near3 stimulating)) same (pig porcine swine)	USPAT; US-PGPUB	2002/05/15 16:36
9	22	((fsh or (follicle near3 stimulating)) same (pig porcine swine)) and litter	USPAT; US-PGPUB	2002/05/15 16:36
10	64	(fsh or (follicle near3 stimulating)) same (allele polymorph\$3 variant snp)	USPAT; US-PGPUB	2002/05/15 16:55
11	19	((fsh or (follicle near3 stimulating)) same (allele polymorph\$3 variant snp)) and (pig porcine litter swine)	USPAT; US-PGPUB	2002/05/15 16:56
12	34	((fsh or (follicle near3 stimulating)) same (allele polymorph\$3 variant snp)) and (pig porcine litter swine)	USPAT; US-PGPUB	2002/05/15 16:56

(FILE 'HOME' ENTERED AT 17:00:41 ON 15 MAY 2002)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 17:00:51 ON 15 MAY 2002
L1 96 SEA PLU=ON (FSH OR (FOLLICLE STIMULAT?)) AND (PIG OR PORCINE
OR SWINE) AND LITTER
L2 59 DUP REM L1 (37 DUPLICATES REMOVED)
L3 15 SEA PLU=ON L1 AND (ALLELE OR POLYMORPH? OR VARIANT OR SNP OR
MUTANT)
L4 11 DUP REM L3 (4 DUPLICATES REMOVED)
D TI 1-11
D IBIB AB 1-11

FILE 'STNGUIDE' ENTERED AT 17:06:53 ON 15 MAY 2002
L5 0 SEA PLU=ON (FSH OR (FOLLICLE STIMULAT?)) AND (PIG OR PORCINE
OR SWINE) AND (OFFSPRING OR PROLIFIC)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 17:18:47 ON 15 MAY 2002

FILE 'AGRICOLA, MEDLINE, BIOSIS, CAPLUS' ENTERED AT 17:18:57 ON 15 MAY
2002
L6 124 SEA PLU=ON (FSH OR (FOLLICLE STIMULAT?)) AND (PIG OR PORCINE
OR SWINE) AND (OFFSPRING OR PROLIFIC OR LITTER)
L7 15 SEA PLU=ON L6 AND (ALLELE OR POLYMORPH? OR VARIANT OR SNP OR
MUTANT)
L8 0 SEA PLU=ON L7 NOT L1
L9 4 SEA PLU=ON L7 NOT L4
D TI 1-4
D IBIB AB 1-4

L2 ANSWER 4 OF 11 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:187644 CAPLUS

DOCUMENT NUMBER: 135:367548

TITLE: The combined genotypes effect of ESR and **FSH**
.beta. genes on **litter** size traits in five
different **pig** breeds

AUTHOR(S): Chen, Kefei; Li, Ning; Huang, Lusheng; Zhang, Qin;
Zhang, Jiansheng; Sun, Shiquan; Luo, Ming; Wu,
Changxin

CORPORATE SOURCE: Provincial Key Laboratory for Animal Biotechnology,
Jiangxi Agricultural University, Nanchang, 330045,
Peop. Rep. China

SOURCE: Chinese Science Bulletin (2001), 46(2), 140-143
CODEN: CSBUEF; ISSN: 1001-6538

PUBLISHER: Science in China Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Estrogen receptor (ESR) and Follicular-stimulating hormone beta subunit (**FSH**.beta.) genes were chosen as candidates to det. whether they control **litter** size and some other reproductive traits in **swine**. 269 Sows from five different **pig** breeds were genotyped by an established PCR-RFLPs protocol at both ESR and **FSH**.beta. loci. The effects of both ESR and **FSH**.beta. on **pig** reproductive traits, including total no. born (TNB) and no. born alive (NBA), are analyzed by SAS software (version 6.12). These computation results demonstrated that both ESR locus and **FSH**.beta. locus are the major genes influencing **litter** size in **pigs**. The sows of BBBB combined genotype of ESR and **FSH**.beta. loci generally produce 1.85-3.01 TNB and 2.0-3.0 NBA more than those of ABAA combined genotype. The notable effect of ESR locus and **FSH**.beta. locus on **litter** size of **pigs** have made it possible to improve the **pig** reprodn. by Marker-assisted selection (MAS). Moreover, introgression of the beneficial **alleles** into com. **pig** breeding lines, in which the **alleles** were not present, will improve greatly the economically important reproductive traits and efficiency of **pig** prodn.

REFERENCE COUNT: 7 THERE ARE 7 CITED R

L2 ANSWER 9 OF 11 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1999:13366 CAPLUS

DOCUMENT NUMBER: 130:247634

TITLE: **FSH**.beta. subunit gene is associated with
major gene controlling **litter** size in
commercial **pig** breeds

AUTHOR(S): Zhao, Yaofeng; Li, Ning; Xiao, Lu; Cao, Gengsheng;
Chen, Yizhen; Zhang, Shun; Chen, Yongfu; Wu,

Changxin;

CORPORATE SOURCE: Zhang, Jiansheng; Sun, Shiquan; Xu, Xueqing
State Key Laboratories Agrobiotechnology, China
Agricultural University, Beijing, 100094, Peop. Rep.
China

SOURCE: Science in China, Series C: Life Sciences (1998),
41(6), 664-668

CODEN: SCCLFO; ISSN: 1006-9305

PUBLISHER: Science in China Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An insertion fragment in **porcine FSH**.beta. subunit
gene was cloned by PCR. Sequencing data show that the insertion is a
retroposon of 292 bp sitting in intron I at the site between +809 and
+810

base. Based on these results, a PCR program was created to genotype
animal individuals in different **pig** breeds at **FSH**
.beta. locus and **polymorphism** of **FSH**.beta. gene was
analyzed. With the combination of genotype and **litter** size of
sows, it was demonstrated that **FSH**.beta. locus is closely
assocd. with major gene controlling **litter** size in com.
pig breeds, such as Yorkshire, Landrace, Durco. Averagely the AA
sows give more 1.5 piglets than BB shows do per **litter**.

REFERENCE COUNT: 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE

FORMAT

L2 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1999:483637 CAPLUS

DOCUMENT NUMBER: 131:320628

TITLE: Relationship between polymerase chain reaction-single strand conformation **polymorphism** (PCR-SSCP) at **FSH** .beta. subunit locus and **litter** size in Erhualian **pig**

AUTHOR(S): Chen, Jie; Jiang, Zhihua; Liu, Honglin; Li, Qixian; Fang, Meiyong; Wu, Yanning

CORPORATE SOURCE: College of Animal Science + Technology, Nanjing Agricultural University, Nanjing, 210095, Peop. Rep. China

SOURCE: Nanjing Nongye Daxue Xuebao (1999), 22(2), 55-58
CODEN: NNDXEI; ISSN: 1000-2030

PUBLISHER: Nanjing Nongye Daxue

DOCUMENT TYPE: Journal

LANGUAGE: Chinese

AB The relationship between PCR-SSCP at **FSH** .beta. subunit locus and **litter** size in Erhualian **pigs** was studied. The large white **pigs** were used as the control breed. Various genotype were found in the Erhualian **pigs**, while only one type in the large white **pigs**. The gene frequency was much different between two breeds at the locus. Variance anal. of **litter** size at the first parity, the sum of the first three parities and the largest parity was done in various genotypes of the Erhualian **pigs**. The results showed there was high linkage between the PCR-SSCP marker and **litter** size.

L2 ANSWER 5 OF 11 MEDLINE DUPLICATE 2
 ACCESSION NUMBER: 2001232441 MEDLINE
 DOCUMENT NUMBER: 21071383 PubMed ID: 11204716
 TITLE: Candidate gene analysis for loci affecting **litter** size and ovulation rate in **swine**.
 AUTHOR: Linville R C; Pomp D; Johnson R K; Rothschild M F
 CORPORATE SOURCE: Department of Animal Science, University of Nebraska, Lincoln 68583-0908, USA.
 SOURCE: JOURNAL OF ANIMAL SCIENCE, (2001 Jan) 79 (1) 60-7. Journal code: HC7; 8003002. ISSN: 0021-8812.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200105
 ENTRY DATE: Entered STN: 20010517
 Last Updated on STN: 20010517
 Entered Medline: 20010503

AB A candidate gene approach was used to determine whether specific loci explain responses in ovulation rate (OR) and number of fully formed (FF), live (NBA), stillborn, and mummified **pigs** at birth observed in two lines selected for ovulation rate and **litter** size compared with a randomly selected control line. Line IOL was selected for an index of OR and embryonic survival for eight generations, followed by eight generations of two-stage selection for OR and **litter** size. Line C was selected at random for 16 generations. Line COL, derived from line

C at Generation 8, underwent eight generations of two-stage selection.

Lines IOL and C differed in mean EBV by 6.1 ova and 4.7 FF, whereas lines COL and C differed by 2.2 ova and 2.9 FF. **Pigs** of Generation 7 of two-stage selection lines were genotyped for the retinol binding protein

4 (RBP4, n = 190) and epidermal growth factor (EGF, n = 189) loci, whereas **pigs** of Generations 7 and 8 were genotyped for the estrogen receptor (ESR, n = 523), prolactin receptor (PRLR, n = 524), **follicle-stimulating** hormone beta (FSHbeta, n = 520), and prostaglandin-endoperoxide synthase 2 (PTGS2, n = 523) loci. Based on chi-square analysis for homogeneity of genotypic frequencies, distributions for PRLR, FSHbeta, and PTGS2 were different among lines (P

< 0.005). Differences in gene frequencies between IOL vs C and COL vs C were

0.33 +/- 0.25 and 0.16 +/- 0.26 for PRLR, 0.35 +/- 0.20 and 0.15 +/- 0.24 for FSHbeta, and 0.16 +/- 0.16 and 0.08 +/- 0.18 for PTGS2. Although

these differences are consistent with a model of selection acting on these loci,

estimates of additive and dominance effects at these loci did not differ from zero (P > 0.05), and several of them had signs inconsistent with the changes in **allele** frequencies. We were not able to find significant associations between the **polymorphic** markers and phenotypes studied; however, we cannot rule out that other genetic variation within these candidate genes has an effect on the traits studied.